Ling Jiang

List of Publications by Year
in descending order

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Version: 2024-02-01

144 papers	8,383 citations	57631 44 h-index	54797 84 g-index
146 all docs	146 docs citations	146 times ranked	6983 citing authors

#	Article	IF	Citations
1	D14â€“SCFD3-dependent degradation of D53 regulates strigolactone signalling. Nature, 2013, 504, 406-410.	13.7	669
2	Isolation and initial characterization of GW5, a major QTL associated with rice grain width and weight. Cell Research, 2008, 18, 1199-1209.	5.7	583
3	DTH8 Suppresses Flowering in Rice, Influencing Plant Height and Yield Potential Simultaneously Â Â. Plant Physiology, 2010, 153, 1747-1758.	2.3	549
4	A Chlorophyll-Deficient Rice Mutant with Impaired Chlorophyllide Esterification in Chlorophyll Biosynthesis. Plant Physiology, 2007, 145, 29-40.	2.3	360
5	A gene cluster encoding lectin receptor kinases confers broad-spectrum and durable insect resistance in rice. Nature Biotechnology, 2015, 33, 301-305.	9.4	299
6	Days to heading 7 , a major quantitative locus determining photoperiod sensitivity and regional adaptation in rice. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16337-16342.	3.3	253
7	A Novel QTL qTGW3 Encodes the GSK3/SHAGGY-Like Kinase OsGSK5/OsSK41 that Interacts with OsARF4 to Negatively Regulate Grain Size and Weight in Rice. Molecular Plant, 2018, 11, 736-749.	3.9	201
8	Ehd4 Encodes a Novel and Oryza-Genus-Specific Regulator of Photoperiodic Flowering in Rice. PLoS Genetics, 2013, 9, e1003281.	1.5	186
9	A Role for a Dioxygenase in Auxin Metabolism and Reproductive Development in Rice. Developmental Cell, 2013, 27, 113-122.	3.1	185
10	Association of functional nucleotide polymorphisms at DTH2 with the northward expansion of rice cultivation in Asia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2775-2780.	3.3	178
11	Disruption of a Rice Pentatricopeptide Repeat Protein Causes a Seedling-Specific Albino Phenotype and Its Utilization to Enhance Seed Purity in Hybrid Rice Production Â Â. Plant Physiology, 2012, 159, 227-238.	2.3	139
12	Rice APC/CTE controls tillering by mediating the degradation of MONOCULM 1. Nature Communications, 2012, 3, 752.	5.8	138
13	An R2R3 MYB transcription factor confers brown planthopper resistance by regulating the phenylalanine ammonia-lyase pathway in rice. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 271-277.	3.3	134
14	STV11 encodes a sulphotransferase and confers durable resistance to rice stripe virus. Nature Communications, 2014, 5, 4768.	5.8	126
15	A novel lipoxygenase gene from developing rice seeds confers dual position specificity and responds to wounding and insect attack. Plant Molecular Biology, 2008, 66, 401-414.	2.0	122
16	A cyclic nucleotide-gated channel mediates cytoplasmic calcium elevation and disease resistance in rice. Cell Research, 2019, 29, 820-831.	5.7	119
17	A Rice Virescent-Yellow Leaf Mutant Reveals New Insights into the Role and Assembly of Plastid Caseinolytic Protease in Higher Plants. Plant Physiology, 2013, 162, 1867-1880.	2.3	116
18	A Novel Chloroplast-Localized Pentatricopeptide Repeat Protein Involved in Splicing Affects Chloroplast Development and Abiotic Stress Response in Rice. Molecular Plant, 2014, 7, 1329-1349.	3.9	114

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19	Pollen Semi-Sterility1Encodes a Kinesin-1â€“Like Protein Important for Male Meiosis, Anther Dehiscence, and Fertility in Rice. Plant Cell, 2011, 23, 111-129.	3.1	113
20	GLUTELIN PRECURSOR ACCUMULATION3Encodes a Regulator of Post-Golgi Vesicular Traffic Essential for Vacuolar Protein Sorting in Rice Endosperm Â. Plant Cell, 2014, 26, 410-425.	3.1	113
21	A selfish genetic element confers non-Mendelian inheritance in rice. Science, 2018, 360, 1130-1132.	6.0	105
22	SLGcontrols grain size and leaf angle by modulating brassinosteroid homeostasis in rice. Journal of Experimental Botany, 2016, 67, 4241-4253.	2.4	103
23	A recruiting protein of geranylgeranyl diphosphate synthase controls metabolic flux toward chlorophyll biosynthesis in rice. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6866-6871.	3.3	101
24	FLOURY ENDOSPERM7encodes a regulator of starch synthesis and amyloplast development essential for peripheral endosperm development in rice. Journal of Experimental Botany, 2016, 67, 633-647.	2.4	91
25	Transcriptional activation and phosphorylation of OsCNGC9 confer enhanced chilling tolerance in rice. Molecular Plant, 2021, 14, 315-329.	3.9	89
26	OsSHI1 Regulates Plant Architecture Through Modulating the Transcriptional Activity of IPA1 in Rice. Plant Cell, 2019, 31, 1026-1042.	3.1	85
27	GOLGI TRANSPORT 1B Regulates Protein Export from the Endoplasmic Reticulum in Rice Endosperm Cells. Plant Cell, 2016, 28, 2850-2865.	3.1	79
28	Young Leaf Chlorosis 1, a chloroplast-localized gene required for chlorophyll and lutein accumulation during early leaf development in rice. Planta, 2013, 237, 279-292.	1.6	78
29	Transcriptional and postâ€transcriptional regulation of heading date in rice. New Phytologist, 2021, 230, 943-956.	3.5	69
30	A comprehensive genetic study reveals a crucial role of <scp>CYP90D2/D2</scp> in regulating plant architecture in rice (<scp>O</scp>ryza sativa). New Phytologist, 2013, 200, 1076-1088.	3.5	68
31	<scp>O</scp>s<scp>ARG</scp> encodes an arginase that plays critical roles in panicle development and grain production in rice. Plant Journal, 2013, 73, 190-200.	2.8	67
32	WSL5, a pentatricopeptide repeat protein, is essential for chloroplast biogenesis in rice under cold stress. Journal of Experimental Botany, 2018, 69, 3949-3961.	2.4	67
33	A knockdown mutation of YELLOW-GREEN LEAF2 blocks chlorophyll biosynthesis in rice. Plant Cell Reports, 2013, 32, 1855-1867.	2.8	64
34	Rice <scp>FLOURY ENDOSPERM</scp>10 encodes a pentatricopeptide repeat protein that is essential for the transâ€splicing of mitochondrial nad1 intron 1 and endosperm development. New Phytologist, 2019, 223, 736-750.	3.5	62
35	ADP-glucose pyrophosphorylase large subunit 2 is essential for storage substance accumulation and subunit interactions in rice endosperm. Plant Science, 2016, 249, 70-83.	1.7	61
36	DEFORMED FLORAL ORGAN1 (DFO1) regulates floral organ identity by epigenetically repressing the expression of OsMADS58 in rice (Oryza sativa). New Phytologist, 2015, 206, 1476-1490.	3.5	56

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37	Marker assisted pyramiding of two brown planthopper resistance genes, Bph3 and Bph27 (t), into elite rice Cultivars. Rice, 2016, 9, 27.	1.7	56
38	OsCNGC13 promotes seed-setting rate by facilitating pollen tube growth in stylar tissues. PLoS Genetics, 2017, 13, e1006906.	1.5	55
39	OsLOX2, a rice type I lipoxygenase, confers opposite effects on seed germination and longevity. Transgenic Research, 2014, 23, 643-655.	1.3	54
40	Brassinosteroids mediate susceptibility to brown planthopper by integrating with the salicylic acid and jasmonic acid pathways in rice. Journal of Experimental Botany, 2018, 69, 4433-4442.	2.4	54
41	Hybrid Sterility in Rice (Oryza sativa L.) Involves the Tetratricopeptide Repeat Domain Containing Protein. Genetics, 2016, 203, 1439-1451.	1.2	52
42	Fine mapping of brown planthopper (Nilaparvata lugens StÃ¥l) resistance gene Bph28(t) in rice (Oryza) Tj ETQq0 0 0 rgBT /Overlock 10	1.0	51
43	High-resolution mapping of brown planthopper (BPH) resistance gene Bph27(t) in rice (Oryza sativa L.). Molecular Breeding, 2013, 31, 549-557.	1.0	50
44	Pyrophosphate: fructose-6-phosphate 1-phosphotransferase (PFP) regulates carbon metabolism during grain filling in rice. Plant Cell Reports, 2016, 35, 1321-1331.	2.8	50
45	FLOURY ENDOSPERM16 encoding a NADâ€dependent cytosolic malate dehydrogenase plays an important role in starch synthesis and seed development in rice. Plant Biotechnology Journal, 2019, 17, 1914-1927.	4.1	50
46	A Point Mutation of Magnesium Chelatase OsCHLI Gene Dampens the Interaction Between CHLI and CHLD Subunits in Rice. Plant Molecular Biology Reporter, 2015, 33, 1975-1987.	1.0	49
47	Postâ€transcriptional regulation of Ghd7 protein stability by phytochrome and Os<scp>GI</scp> in photoperiodic control of flowering in rice. New Phytologist, 2019, 224, 306-320.	3.5	48
48	The catalytic subunit of magnesium-protoporphyrin IX monomethyl ester cyclase forms a chloroplast complex to regulate chlorophyll biosynthesis in rice. Plant Molecular Biology, 2016, 92, 177-191.	2.0	47
49	Disruption of gene <scp>SPL</scp>35, encoding a novel <scp>CUE</scp> domainâ€containing protein, leads to cell death and enhanced disease response in rice. Plant Biotechnology Journal, 2019, 17, 1679-1693.	4.1	46
50	Rice stripe virus suppresses jasmonic acid-mediated resistance by hijacking brassinosteroid signaling pathway in rice. PLoS Pathogens, 2020, 16, e1008801.	2.1	45
51	Discovery of broad-spectrum fungicides that block septin-dependent infection processes of pathogenic fungi. Nature Microbiology, 2020, 5, 1565-1575.	5.9	44
52	The role of OsMSH4 in male and female gamete development in rice meiosis. Journal of Experimental Botany, 2016, 67, 1447-1459.	2.4	43
53	CRL6, a member of the CHD protein family, is required for crown root development in rice. Plant Physiology and Biochemistry, 2016, 105, 185-194.	2.8	42
54	Overexpression of OsbHLH107, a member of the basic helix-loop-helix transcription factor family, enhances grain size in rice (Oryza sativa L.). Rice, 2018, 11, 41.	1.7	42

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55	Construction of a new set of rice chromosome segment substitution lines and identification of grain weight and related traits QTLs. Breeding Science, 2010, 60, 305-313.	0.9	40
56	Small grain and semi-dwarf 3, a WRKY transcription factor, negatively regulates plant height and grain size by stabilizing SLR1 expression in rice. Plant Molecular Biology, 2020, 104, 429-450.	2.0	40
57	<scp>DELAYED HEADING DATE</scp>1 interacts with Os<scp>HAP</scp>5C/D, delays flowering time and enhances yield in rice. Plant Biotechnology Journal, 2019, 17, 531-539.	4.1	39
58	WRKY Transcription Factor OsWRKY29 Represses Seed Dormancy in Rice by Weakening Abscisic Acid Response. Frontiers in Plant Science, 2020, 11, 691.	1.7	38
59	Isolation and characterization of a spotted leaf 32 mutant with early leaf senescence and enhanced defense response in rice. Scientific Reports, 2017, 7, 41846.	1.6	37
60	Identification of QTLs for seed dormancy in rice (Oryza sativa L.). Plant Breeding, 2011, 130, 328-332.	1.0	36
61	Imidacloprid is degraded by CYP353D1v2, a cytochrome P450 overexpressed in a resistant strain of Laodelphax striatellus. Pest Management Science, 2017, 73, 1358-1363.	1.7	36
62	Os<scp>PEX</scp>5 regulates rice spikelet development through modulating jasmonic acid biosynthesis. New Phytologist, 2019, 224, 712-724.	3.5	36
63	Earlier Degraded Tapetum1 (EDT1) Encodes an ATP-Citrate Lyase Required for Tapetum Programmed Cell Death. Plant Physiology, 2019, 181, 1223-1238.	2.3	34
64	Breeding strategies for optimum heading date using genotypic information in rice. Molecular Breeding, 2010, 25, 287-298.	1.0	33
65	Identification of quantitative trait loci for seed storability in rice (Oryza sativa L.). Plant Breeding, 2012, 131, 739-743.	1.0	32
66	Gene SGL, encoding a kinesin-like protein with transactivation activity, is involved in grain length and plant height in rice. Plant Cell Reports, 2014, 33, 235-244.	2.8	32
67	TheRICE MINUTE-LIKE1(RML1) gene, encoding a ribosomal large subunit protein L3B, regulates leaf morphology and plant architecture in rice. Journal of Experimental Botany, 2016, 67, 3457-3469.	2.4	32
68	EF8 is involved in photoperiodic flowering pathway and chlorophyll biogenesis in rice. Plant Cell Reports, 2014, 33, 2003-2014.	2.8	31
69	Mapping QTLs related to rice seed storability under natural and artificial aging storage conditions. Euphytica, 2015, 203, 673-681.	0.6	30
70	WSL3, a component of the plastid-encoded plastid RNA polymerase, is essential for early chloroplast development in rice. Plant Molecular Biology, 2016, 92, 581-595.	2.0	30
71	Disruption of OsARF19 is Critical for Floral Organ Development and Plant Architecture in Rice (Oryza) Tj ETQq1 1 0.784314 rgBT /Ove	1.0	30
72	Mapping two major effect grain dormancy QTL in rice. Molecular Breeding, 2011, 28, 453-462.	1.0	29

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73	FLOURY ENDOSPERM15 encodes a glyoxalase I involved in compound granule formation and starch synthesis in rice endosperm. Plant Cell Reports, 2019, 38, 345-359.	2.8	27
74	Loss of Function of the Cytochrome P450 Gene CYP78B5 Causes Giant Embryos in Rice. Plant Molecular Biology Reporter, 2015, 33, 69-83.	1.0	26
75	SGD1, a key enzyme in tocopherol biosynthesis, is essential for plant development and cold tolerance in rice. Plant Science, 2017, 260, 90-100.	1.7	26
76	OsPKpÎ±1 encodes a plastidic pyruvate kinase that affects starch biosynthesis in the rice endosperm. Journal of Integrative Plant Biology, 2018, 60, 1097-1118.	4.1	26
77	DHD4, a CONSTANS-like family transcription factor, delays heading date by affecting the formation of the FAC complex in rice. Molecular Plant, 2021, 14, 330-343.	3.9	26
78	The Origin of Weedy Rice Ludao in China Deduced by Genome Wide Analysis of Its Hybrid Sterility Genes. Breeding Science, 2005, 55, 409-414.	0.9	25
79	Marker-assisted breeding of a photoperiod-sensitive male sterile japonica rice with high cross-compatibility with indica rice. Molecular Breeding, 2011, 27, 247-258.	1.0	25
80	Molecular genetic characterization of rice seed lipoxygenase 3 and assessment of its effects on seed longevity. Journal of Plant Biology, 2013, 56, 232-242.	0.9	24
81	Plastidial Disproportionating Enzyme Participates in Starch Synthesis in Rice Endosperm by Transferring Maltooligosyl Groups from Amylose and Amylopectin to Amylopectin. Plant Physiology, 2015, 169, pp.01411.2015.	2.3	24
82	OsVIN2 encodes a vacuolar acid invertase that affects grain size by altering sugar metabolism in rice. Plant Cell Reports, 2019, 38, 1273-1290.	2.8	24
83	Rice FLOURY ENDOSPERM 18 encodes a pentatricopeptide repeat protein required for 5â€² processing of mitochondrial nad5 messenger RNA and endosperm development. Journal of Integrative Plant Biology, 2021, 63, 834-847.	4.1	24
84	white panicle2 encoding thioredoxin z, regulates plastid RNA editing by interacting with multiple organellar RNA editing factors in rice. New Phytologist, 2021, 229, 2693-2706.	3.5	24
85	Identification of a new hybrid sterility gene in rice (bi Oryza sativa L.). Euphytica, 2006, 151, 331-337.	0.6	23
86	Genetic dissection of seed storability using two different populations with a same parent rice cultivar N22. Breeding Science, 2015, 65, 411-419.	0.9	23
87	OPEN GLUME1: a key enzyme reducing the precursor of JA, participates in carbohydrate transport of lodicules during anthesis in rice. Plant Cell Reports, 2018, 37, 329-346.	2.8	23
88	Young Seedling Stripe1 encodes a chloroplast nucleoid-associated protein required for chloroplast development in rice seedlings. Planta, 2017, 245, 45-60.	1.6	22
89	Early heading 7 interacts with DTH8, and regulates flowering time in rice. Plant Cell Reports, 2019, 38, 521-532.	2.8	22
90	FLOURY ENDOSPERM12 Encoding Alanine Aminotransferase 1 Regulates Carbon and Nitrogen Metabolism in Rice. Journal of Plant Biology, 2019, 62, 61-73.	0.9	22

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91	OsDOG1L-3 regulates seed dormancy through the abscisic acid pathway in rice. Plant Science, 2020, 298, 110570.	1.7	21
92	Identification of Quantitative Trait Loci Associated with Aluminum Tolerance in Rice (Oryza Sativa L.). Euphytica, 2006, 150, 37-45.	0.6	20
93	Plastidic pyruvate dehydrogenase complex E1 component subunit Alpha1 is involved in galactolipid biosynthesis required for amyloplast development in rice. Plant Biotechnology Journal, 2022, 20, 437-453.	4.1	20
94	Dwarf and tiller-enhancing 1 regulates growth and development by influencing boron uptake in boron limited conditions in rice. Plant Science, 2015, 236, 18-28.	1.7	19
95	Identification of quantitative trait loci for resistance to rice black-streaked dwarf virus disease and small brown planthopper in rice. Molecular Breeding, 2017, 37, 1.	1.0	18
96	Deltamethrin is metabolized by CYP6FU1, a cytochrome P450 associated with pyrethroid resistance, in <scp>Laodelphax striatellus</scp>. Pest Management Science, 2018, 74, 1265-1271.	1.7	18
97	Post-Golgi trafficking of rice storage proteins requires the small GTPase Rab7 activation complex MON1â€“CCZ1. Plant Physiology, 2021, 187, 2174-2191.	2.3	17
98	Lethal albinic seedling, encoding a threonyl-tRNA synthetase, is involved in development of plastid protein synthesis system in rice. Plant Cell Reports, 2017, 36, 1053-1064.	2.8	16
99	Fine mapping of S37, a locus responsible for pollen and embryo sac sterility in hybrids between Oryza sativa L. and O. glaberrima Steud. Plant Cell Reports, 2015, 34, 1885-1897.	2.8	14
100	Microarray-based gene expression analysis of strong seed dormancy in rice cv. N22 and less dormant mutant derivatives. Plant Physiology and Biochemistry, 2016, 99, 27-38.	2.8	14
101	Top Bending Panicle1 is involved in brassinosteroid signaling and regulates the plant architecture in rice. Plant Physiology and Biochemistry, 2017, 121, 1-13.	2.8	14
102	Du13 encodes a C₂H₂ zincâ€finger protein that regulates Wx^b preâ€mRNA splicing and microRNA biogenesis in rice endosperm. Plant Biotechnology Journal, 2022, 20, 1387-1401.	4.1	14
103	Mapping QTL for Seed Dormancy in Weedy Rice. Acta Agronomica Sinica, 2008, 34, 737-742.	0.3	12
104	Fine mapping of a gene causing hybrid pollen sterility between Yunnan weedy rice and cultivated rice (Oryza sativa L.) and phylogenetic analysis of Yunnan weedy rice. Planta, 2010, 231, 559-570.	1.6	12
105	Identification and Phenotypic Characterization of ZEBRA LEAF16 Encoding a Î²-Hydroxyacyl-ACP Dehydratase in Rice. Frontiers in Plant Science, 2018, 9, 782.	1.7	12
106	Transcriptomics Analysis Identified Candidate Genes Colocalized with Seed Dormancy QTLs in Rice (Oryza sativa L.). Journal of Plant Biology, 2010, 53, 330-337.	0.9	11
107	Mapping of quantitative trait loci associated with rice black-streaked dwarf virus disease and its insect vector in rice (Oryza sativa L.). Plant Breeding, 2018, 137, 698-705.	1.0	11
108	A GARP transcription factor anther dehiscence defected 1 (OsADD1) regulates rice anther dehiscence. Plant Molecular Biology, 2019, 101, 403-414.	2.0	11

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109	Genome-wide association study and linkage analysis on resistance to rice black-streaked dwarf virus disease. Molecular Breeding, 2019, 39, 1.	1.0	11
110	Rice albino 1, encoding a glycyl-tRNA synthetase, is involved in chloroplast development and establishment of the plastidic ribosome system in rice. Plant Physiology and Biochemistry, 2019, 139, 495-503.	2.8	11
111	A Natural Variation in PLEIOTROPIC DEVELOPMENTAL DEFECTS Uncovers a Crucial Role for Chloroplast tRNA Modification in Translation and Plant Development. Plant Cell, 2020, 32, 2345-2366.	3.1	11
112	Rice OsBT1 regulates seed dormancy through the glycometabolism pathway. Plant Physiology and Biochemistry, 2020, 151, 469-476.	2.8	11
113	Identification of Japonica Chromosome Segments Associated with Heterosis for Yield in Indica Ã— Japonica Rice Hybrids. Crop Science, 2010, 50, 2328-2337.	0.8	10
114	Quantitative trait loci for grain-quality traits across a rice F2 population and backcross inbred lines. Euphytica, 2013, 192, 25-35.	0.6	10
115	Decreased grain size1, a C3HC4-type RING protein, influences grain size in rice (Oryza sativa L.). Plant Molecular Biology, 2021, 105, 405-417.	2.0	10
116	The Identification and Mapping of a Tiller Angle QTL on Rice Chromosome 9. Crop Science, 2008, 48, 1799-1806.	0.8	9
117	Fine mapping of a gene responsible for pollen semi-sterility in hybrids between Oryza sativa L. and O. glaberrima Steud. Molecular Breeding, 2011, 28, 323-334.	1.0	9
118	Fine mapping of a minor-effect QTL, DTH12, controlling heading date in rice by up-regulation of florigen genes under long-day conditions. Molecular Breeding, 2014, 34, 311-322.	1.0	9
119	A Critical Role of OsMADS1 in the Development of the Body of the Palea in Rice. Journal of Plant Biology, 2018, 61, 11-24.	0.9	8
120	Identification of QTL for seed dormancy from weedy rice and its application to elite rice cultivar â€˜Ninggeng 4â€™. Molecular Breeding, 2019, 39, 1.	1.0	8
121	Purine nucleotide biosynthetic gene GARS controls early chloroplast development in rice (Oryza) Tj ETQq1 1 0.784314 rgBT /Overlock	2.8	8
122	Genetic Analysis of Two Weak Dormancy Mutants Derived from Strong Seed Dormancy Wild Type Rice N22 (Oryza sativa)F. Journal of Integrative Plant Biology, 2011, 53, 338-346.	4.1	7
123	RiceSTOMATAL CYTOKINESIS DEFECTIVE2regulates cell expansion by affecting vesicular trafficking in rice. Plant Physiology, 2022, 189, 567-584.	2.3	7
124	Genotyping the Heading Date of Male-Sterile Rice Line II-32A. Journal of Integrative Plant Biology, 2006, 48, 440-446.	4.1	6
125	The Inheritance of Early Heading in the Rice Variety USSR5. Journal of Genetics and Genomics, 2007, 34, 46-55.	1.7	6
126	Genetic dissection of leaf-related traits using 156 chromosomal segment substitution lines. Journal of Plant Biology, 2015, 58, 402-410.	0.9	6

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127	Identification and fine mapping of qWBPH11 conferring resistance to whitebacked planthopper (Sogatella furcifera Horvath) in rice (Oryza sativa L.). Molecular Breeding, 2018, 38, 1.	1.0	6
128	ENLARGED STARCH GRAIN1 affects amyloplast development and starch biosynthesis in rice endosperm. Plant Science, 2021, 305, 110831.	1.7	6
129	WSL9 Encodes an HNH Endonuclease Domain-Containing Protein that Is Essential for Early Chloroplast Development in Rice. Rice, 2020, 13, 45.	1.7	6
130	Genotypes of Heading Date of Middle Indica Rice in the Midâ€lower Region of the Yangtze River. Journal of Integrative Plant Biology, 2007, 49, 1772-1781.	4.1	5
131	A new gene controlling hybrid sterility in rice (Oryza sativa L.). Euphytica, 2012, 184, 15-22.	0.6	5
132	Semidwarf gene <scp>sdk</scp> has pleiotropic effects on rice (<scp>O</scp>ryza sativa) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.0	5
133	Fine mapping of <scp>qSS</scp>â€9, a major and stable quantitative trait locus, for seed storability in rice (Oryza sativa L.). Plant Breeding, 2015, 134, 293-299.	1.0	5
134	Fine mapping of DTH3b, a minor heading date QTL potentially functioning upstream of Hd3a and RFT1 under long-day conditions in rice. Molecular Breeding, 2015, 35, 1.	1.0	5
135	Nuclear encoded elongation factor EF-Tu is required for chloroplast development in rice grown under low-temperature conditions. Journal of Genetics and Genomics, 2022, 49, 502-505.	1.7	5
136	Genetic analysis and fine mapping of a dominant dwarfness gene from wild rice (Oryza barthii). Plant Breeding, 2018, 137, 50-59.	1.0	4
137	QTL mapping for resistance to strip virus disease in rice. Plant Breeding, 2011, 130, 321-327.	1.0	3
138	Detection and fine mapping of two quantitative trait loci for partial resistance to stripe virus in rice (Oryza sativa L.). Molecular Breeding, 2012, 30, 1379-1391.	1.0	3
139	Knock-down of OsLOX by RNA interference leads to improved seed viability in rice. Journal of Plant Biology, 2015, 58, 293-302.	0.9	3
140	Construction and evaluation of introgression lines and fine mapping of ehd8 from Jinghong common wild rice (Oryza rufipogon). Plant Breeding, 2019, 138, 163-173.	1.0	3
141	Fine mapping of qSdr9, a novel locus for seed dormancy (SD) in weedy rice, and development of NILs with a strong SD allele. Molecular Breeding, 2020, 40, 1.	1.0	3
142	Identification of Quantitative Trait Loci Affecting Grain Fat Content in Rice (Oryza sativa L.). Cereal Chemistry, 2010, 87, 118-124.	1.1	2
143	OsLUGL is involved in the regulating auxin level and OsARFs expression in rice (Oryza sativa L.). Plant Science, 2019, 288, 110239.	1.7	2
144	Assembly and phylogenetic analysis of the complete chloroplast genome sequence of Actinidia setosa. Mitochondrial DNA Part B: Resources, 2019, 4, 3679-3680.	0.2	1